

IDENTIFIED LAB mRNA SEQUENCES

1. The first step is to identify the problem or question that needs to be addressed. This involves understanding the context and the specific requirements of the task.

GOLD

{Stop Codon}

{Instability Sequence}

{Instability Sequence}

(Instability Sequence)

(Instability Sequence)

{Sub-optimal Poly-
adenylation Site}

{Optimal Polyadeny-
lation Site}

Figure 2

COMPUTER PREDICTED DOMAINS
IN LABYRINTHIN

MVIALLCVWTSVAWVFDLVDYEEVLGKLGIYDADGDGDFDVDDAKVLLGLK

ERSTSEPAVPPEEAEPHTEPEEQVPVEAEPQNIIEDEAKEQIQSLLHEMVHAE

HVEGEDLQQEDGPTGEPQQEDDEFILMATDVDDRFEFETLEPEVSHEETEHSYHV

EETVSQDCNQDMEEMMSEQENPDSSEPVVEDERLHHDTDVtyqvyeegavY

<---MAD I--->

EPLENEGIEITEVTAPPEDNPVEDSQviveevsifpvEEQQEVPPDT

<---MAD VII-->

Predicted Ca⁺⁺ Binding Region

VLGKLGIYDADGDGDFDVDDAKVLLGLK

Parvalbumin
Calmodulin
Troponin-C

vkka~~fai~~**ldgdksgf**~~ie~~**edelklfl**qnf
~~fke~~**afslfdk**~~gdgt~~**tittkelgtv**mrsl
~~ladc~~**frufaknadg**~~fidie~~**elge**ilrat

Ca⁺⁺ Binding Residues
Required residue

* * * * *

+

SYMBOL KEY

BOLD = Eukaryotic Leader Sequence

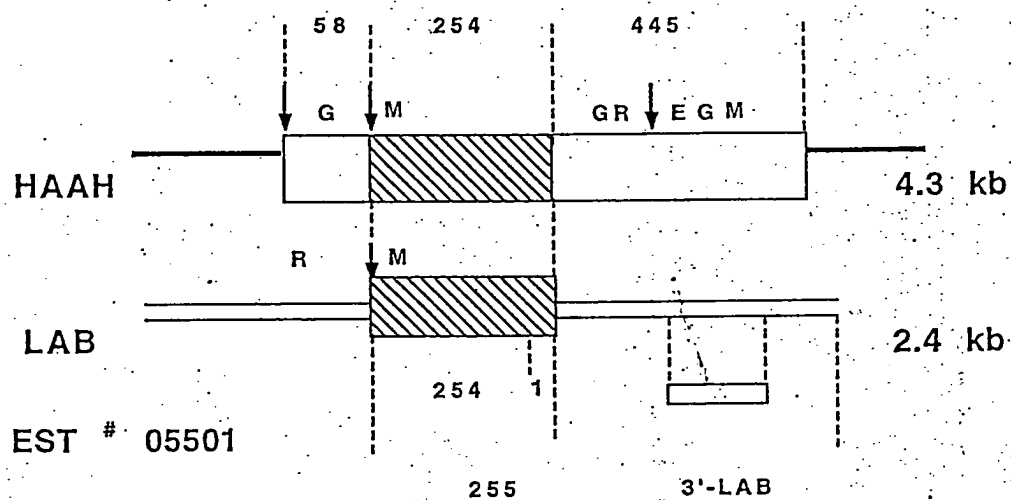
_____ = Myristylation site

^
lower case = Membrane Anchoring Domain (MAD)

<----->

364763 540000

Figure 3



↓ = Start Codon
 R = Ribosome Binding Site
 E = Enzymatic Site
 G = Glycosylation Site
 M = Membrane Anchoring Domain
 3'-LAB = Contains poly A signal (x2); instability sequence (x4)

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